

In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 37, lines 3-5 and replace it with the following paragraph:

Low complexity sequence found by a filter program is substituted using the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNNN") (SEQ ID NO: 1) and the letter "X" in protein sequences (e.g., "XXXXXXXXXX") (SEQ ID NO: 2).

Please delete the paragraph on page 39, lines 6-16 and replace it with the following paragraph:

Five polypeptides, fragments, homologues, variants and derivatives, are typically made by recombinant means, for example as described below in the Examples. However they may also be made by synthetic means using techniques well known to skilled persons such as solid phase synthesis. The proteins may also be produced as fusion proteins, for example to aid in extraction and purification. Examples of fusion protein partners include glutathione-S-transferase (GST), 6xHis (SEQ ID NO: 488), GAL4 (DNA binding and/or transcriptional activation domains) and β -galactosidase. It may also be convenient to include a proteolytic cleavage site between the fusion protein partner and the protein sequence of interest to allow removal of fusion protein sequences. Preferably the fusion protein will not hinder the function of the protein of interest sequence. Proteins may also be obtained by purification of cell extracts from animal cells.

Please delete the paragraph on page 137, lines 18-26 and replace it with the following paragraph:

The DNA fragment encoding E7 of HPV type 16 is subcloned into pGEX-4T1 protein expression vector. E7 DNA fragment is amplified by polymerase chain reaction (PCR) using a set of primers: 5'-TTGTTGGATCCCATGGAGATACACCTACATTG-3' (**SEQ ID NO: 3**) and 5'-TTACTGAATTCTTATGGTTTCTGAGAACAGATG-3' (**SEQ ID NO: 4**). The amplified DNA is digested with BamH1 and EcoR1, and the resulting fragment is then cloned into the BamH1 and EcoR1 sites of pGEX- 4T1 vector. The presence of the inserted E7 is confirmed by and restriction enzyme digestion and gel electrophoresis. The accuracy of the constructs is further confirmed by DNA sequencing. The plasmid construct is transformed into Escherichia coli TG-1 for protein expression.

Please delete Appendix A on pages 160-171, and replace it with the following Appendix:

Appendix A: Sequences

Fve is isolated from Golden Needle Mushroom (*Flammulina velutipes*). ORGANISM: *Flammulina velutipes*. Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales; Tricholomataceae; *Flammulina*.

Fve (Wild type)

ATGTCGCCACGTCGCTCACCTTCCAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCC
CAACTGGGGCCGTGGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCAGACA
AAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACA
CCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAACAAGGGGTATGGTGTCGCGGACACCAAAC
GATTCAAGTTTTCTGTTGTTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGAAGA
AGACTTGA (**SEQ ID NO: 5**)
msatsltfqlaylvkkidfdytpnwgrgtppssyidnltfpkvltdkkysyrvvngsdlgvesnfavt
psggqtinlfqynkgygvadtktiqvfvpipdtgnseeiiaewkkt (**SEQ ID NO: 6**)
ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA (**SEQ ID NO: 5**)

A Fve (Wild type) sequence may also comprise a sequence as set out above, but lacking the initial methionine (M) in the amino acid sequence, or lacking the initial ATG in the nucleic acid sequence.

GST-Fve (Wild type) Nucleotide Sequence

ATGTCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCACTCGACTTCTTTT
GGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAAATGGC
GAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGAT
GTTAAATTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACACATGTTGGG
TGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGTTTTTGGATATTAGAT
ACGGTGTTCGAGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGC
AAGCTACCTGAAATGCTGAAAATGTTTGAAGATCGTTTATGTCATAAAACATATTTAAATGG
TGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGG
ACCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAAAACGTATTGAAGCTATC
CCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCA
AGCCACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGAAGTTCTGTTCCAGGGGC
CCCTGGGATCCTCCGCCACGTCGCTCACCTTCCAGCTTGCCTACTTGGTGAAGAAGATCGAC
TTCGACTACACCCCCAACTGGGGCCGTGGTACCCCAAGCAGCTACATCGACAACCTTACCTT
CCCCAAGGTTCTCACCGACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTG
GCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCTCCAGTAC
AACAAGGGGTATGGTGTGCGCGACACCAAAACGATTCAAGTTTTCGTTGTCATTCCAGATAC
CGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 7)**

GST-Fve (Wild type) Amino Acid Sequence

MSPI LGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQS
MAIIRYIADKHNMLGGCPKERA EISMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPEMLKMFEDR
LCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAI PQIDKYLKSSKYIAWPLQ
GWQATFGGGDHPPKSDLEVL FQG PLGSSATSLTFQLAYLVKKIDFDYTPNWGRGTPSSYIDNLTfPKV
LTDKKYSYRVVNGSDLGVESNF AVTPSGGQTINFLQYNKG YGVADTKTIQVFVVIPDTGNSE EYIIA
EWKKT **(SEQ ID NO: 8)**

FVE DELETION MUTANTS

Fve D6-18

ATG/TCC/GCC/ACG/TCG/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/
AGC/AGC/TAC/ATC/GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/
TAC/TCG/TAC/CGC/GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/
TTC/GCA/GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/
AAG/GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/
CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/
TGA **(SEQ ID NO: 9)**

msats/fdytpnwgrgtpssyidnltfpkvlt dkkysyrvvngsdlgvesnfavtpsggqtinflqy
nkg ygvadtktiqvf vvipdtgnseeyiiaewkkt **(SEQ ID NO: 10)**

Fve D19-33

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/ATC/GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/
TAC/CGC/GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/
GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/
TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/
ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ**
ID NO: 11)

msatsltfqlaylvkkid/idnltpkvltdkkysyrvvngsdlgvesnfavtpsggqtnflqynk
gygvadtktiqvfvpdtdgnseeiiaewkkt **(SEQ ID NO: 12)**

Fve D34-46

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/AAA/
TAC/TCG/TAC/CGC/GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/
TTC/GCA/GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/
AAG/GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/
CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/
TGA **(SEQ ID NO: 13)**

msatsltfqlaylvkkidfdytpnwgrgtpssy/kysyrvvngsdlgvesnfavtpsggqtnflqy
nkgygvadtktiqvfvpdtdgnseeiiaewkkt **(SEQ ID NO: 14)**

Fve D47-60

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/GTC/GAG/TCC/AAC/TTC/
GCA/GTG/ACA/CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/
GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/
GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA
(SEQ ID NO: 15)

msatsltfqlaylvkkidfdytpnwgrgtpssyidnltpkvltdk/vesnfavtpsggqtnflqyn
kgygvadtktiqvfvpdtdgnseeiiaewkkt **(SEQ ID NO: 16)**

Fve D61-72

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/
AAC/AAG/GGG/TAT/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/
ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/
ACT/TGA **(SEQ ID NO: 17)**

msatsltfqlaylvkkidfdytpnwgrgtpssyidnltpkvltdkkysyrvvngsdlg/qtinflq
ynkgygvadtktiqvfvpdtdgnseeiiaewkkt **(SEQ ID NO: 18)**

Fve D73-84

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/
CCG/TCC/GGT/GGG/GGT/GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/

ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/
ACT/TGA **(SEQ ID NO: 19)**
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlgvesnfavt
psgg/gvadtktiqvfvipdtgnseeiyiaewkkt **(SEQ ID NO: 20)**

Fve D85-97

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GTC/
ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/
ACT/TGA **(SEQ ID NO: 21)**
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlgvesnfavt
psgggtinlqynkgy/ipdtgnseeiyiaewkkt **(SEQ ID NO: 22)**

Fve D98-106

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/TAC/ATC/ATC/GCT/GAG/
TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 23)**
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlgvesnfavt
psgggtinlqynkgygvadtktiqvfvyiaewkkt **(SEQ ID NO: 24)**

Fve D107-115

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/
AAC/TCG/GAG/GAG/TGA **(SEQ ID NO: 25)**
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlgvesnfavt
psgggtinlqynkgygvadtktiqvfvipdtgnsee/ **(SEQ ID NO: 26)**

Fve D61-97

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/ATT/CCA/GAT/ACC/GGC/AAC/TCG/GAG/
GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 27)**
msatsltfqlaylvkkidfdytpnwgrgtpssyidnltfpkvltdkkysyrvvvngsdlg/ipdtgns
eeyiaewkkt **(SEQ ID NO: 28)**

Fve p55-100

AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/CCG/TCC/GGT/
GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/GTC/GCG/GAC/
ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ **(SEQ ID NO: 29)**
Ngsdlgvesnfavtpsgggtinflqynkgygvadtktiqvfvipd **(SEQ ID NO: 30)**

FVE MUTANTS WITH SINGLE AMINO ACID SUBSTITUTIONS

FveR27A

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/**GCA**/GGT/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 31)**
msatsltfqlaylvkkidfdytpnwga**g**atpssyidnltfpkvltddkysyrvvngsdlgvesnfavt
psgggtinflqynkgygvadtktiqvfvipdtgnseeyiaewkkt **(SEQ ID NO: 32)**

FveG28A

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/**GCA**/ACC/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 33)**
msatsltfqlaylvkkidfdytpnwgr**a**tppssyidnltfpkvltddkysyrvvngsdlgvesnfavt
psgggtinflqynkgygvadtktiqvfvipdtgnseeyiaewkkt **(SEQ ID NO: 34)**

FveT29A

ATG/TCC/GCC/ACG/TCG/CTC/ACC/TTC/CAG/CTT/GCC/TAC/TTG/GTG/AAG/AAG/ATC/
GAC/TTC/GAC/TAC/ACC/CCC/AAC/TGG/GGC/CGT/GGT/**GCA**/CCA/AGC/AGC/TAC/ATC/
GAC/AAC/CTT/ACC/TTC/CCC/AAG/GTT/CTC/ACC/GAC/AAA/AAA/TAC/TCG/TAC/CGC/
GTC/GTG/GTC/AAT/GGC/TCT/GAC/CTT/GGC/GTC/GAG/TCC/AAC/TTC/GCA/GTG/ACA/
CCG/TCC/GGT/GGG/CAG/ACC/ATC/AAC/TTC/CTC/CAG/TAC/AAC/AAG/GGG/TAT/GGT/
GTC/GCG/GAC/ACC/AAA/ACG/ATT/CAA/GTT/TTC/GTT/GTC/ATT/CCA/GAT/ACC/GGC/
AAC/TCG/GAG/GAG/TAC/ATC/ATC/GCT/GAG/TGG/AAG/AAG/ACT/TGA **(SEQ ID NO: 35)**
msatsltfqlaylvkkidfdytpnwgr**a**pssyidnltfpkvltddkysyrvvngsdlgvesnfavt
psgggtinflqynkgygvadtktiqvfvipdtgnseeyiaewkkt **(SEQ ID NO: 36)**

FUSION PROTEINS OF MAJOR HOUSE DUST MITE ALLERGEN (BLO T 5 OR DER P 2) AND FUNGAL IMMUNOMODULATORY PROTEIN FVE

Blo t 5-Fve (two-in-one chimeric wild type)

caagagcacaagccaaagaaggatgatttccgaaacgaattcgatcacttggtgatcgaacaggcaaa
ccatgctatcgaaaagggagaaacatcaattgctttacttgcaacaccaactcgacgaattgaatgaaa
acaagagcaaggaattgcaagagaaaaatcattcgagaacttgatggtggttgcgccatgatcgaagga
gccaaggagctttggaacgtgaattgaagcgaactgatcttaacattttggaacgattcaactacga
agaggctcaaactctcagcaagatcttgcttaaggatttgaaggaaaccgaacaaaaagtgaaggata
ttcaaaccctaaTCCGCCACGTCGCTCACCTTCCAGCTTGCTTACTTGGTGAAGAAGATCGACTTCGAC
TACACCCCCAACTGGGGCCGTGGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCT
CACCGACAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCG
CAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGAC
ACCAAAACGATTCAAGTTTTTCGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTGA
GTGGAAGAAGACTTGA **(SEQ ID NO: 37)**

QEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQLDENENKSKELQEKIIRELDVVCAMIEG
AQGALERELKRTDLNILERFNYYEAAQTLKILLKDLKETEQKVKDIQTQsatsltfqlaylvkkidfd
ytpnwgrgtpssyidnltfpkvltddkysyrvvngsdlgvesnfavtppsggqtinflqynkgygvad
tktiqvfvvipdtgnseeyiaewkkt **(SEQ ID NO: 38)**

Blo t 5-FveR27A (two-in-one chimeric mutant)

caagagcacaagccaaagaaggatgatttccgaaacgaattcgatcacttggtgatcgaacaggcaaa
ccatgctatcgaaaagggagaaacatcaattgctttacttgcaacaccaactcgacgaattgaatgaaa
acaagagcaaggaattgcaagagaaaaatcattcgagaacttgatggtggttgcgccatgatcgaagga
gccaaggagctttggaacgtgaattgaagcgaactgatcttaacattttggaacgattcaactacga
agaggctcaaactctcagcaagatcttgcttaaggatttgaaggaaaccgaacaaaaagtgaaggata
ttcaaaccctaaTCCGCCACGTCGCTCACCTTCCAGCTTGCTTACTTGGTGAAGAAGATCGACTTCGAC
TACACCCCCAACTGGGGC**GCA**GGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTTC
TCACCGACAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTC
GCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGA
CACCAAAACGATTCAAGTTTTTCGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTG
AGTGGAAGAAGACTTGA **(SEQ ID NO: 39)**

QEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQLDENENKSKELQEKIIRELDVVCAMIEG
AQGALERELKRTDLNILERFNYYEAAQTLKILLKDLKETEQKVKDIQTQsatsltfqlaylvkkidfd
ytpnwga**g**tpssyidnltfpkvltddkysyrvvngsdlgvesnfavtppsggqtinflqynkgygvad
tktiqvfvvipdtgnseeyiaewkkt **(SEQ ID NO: 40)**

Blo t 5-FveT29A (two-in-one chimeric mutant)

caagagcacaagccaaagaaggatgatttccgaaacgaattcgatcacttggtgatcgaacaggcaaa
ccatgctatcgaaaagggagaaacatcaattgctttacttgcaacaccaactcgacgaattgaatgaaa
acaagagcaaggaattgcaagagaaaaatcattcgagaacttgatggtggttgcgccatgatcgaagga
gccaaggagctttggaacgtgaattgaagcgaactgatcttaacattttggaacgattcaactacga
agaggctcaaactctcagcaagatcttgcttaaggatttgaaggaaaccgaacaaaaagtgaaggata
ttcaaaccctaaTCCGCCACGTCGCTCACCTTCCAGCTTGCTTACTTGGTGAAGAAGATCGACTTCGAC
TACACCCCCAACTGGGGCCGTGGT**GCA**CCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTTC
TCACCGACAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTC
GCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGA
CACCAAAACGATTCAAGTTTTTCGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTG
AGTGGAAGAAGACTTGA **(SEQ ID NO: 41)**

QEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQDELNENKSKELQEKIIRELDVVCAMIEG
AQGALERELKRTDLNILERFNYEEAQTLSKILLKDLKETEQKVVDIQTQsatsltfqlaylvkkidfd
ytpnwgrg**a**pssyidnltfpkvltddkysyrvvngsdlgvesnfavtspgggtinflqynkgygvad
tktiqvfvpdgtgnseeyiaewkkt **(SEQ ID NO: 42)**

Der p 2-FveR27A (two-in-one chimeric mutant)

gatcaagtcgatgtcaaagattgtgccaatcatgaaatcaaaaaagttttggtaccaggatgccatgg
ttcagaaccatgtatcattcatcggtgtaaacattccaattggaagccgttttcgaagccaacaaa
acacaaaaacggctaaaattgaaatcaaagcctcaatcgatggtttagaagttgatgttcccggatc
gatccaaatgcatgccattacatgaaatgccattggttaaaggacaacaatatgatattaaatatac
atggaatgttccgaaaattgcacaaaaatctgaaaatggtgtcgctcactgttaaagttatgggtgatg
atggtgttttggcctgtgctattgctactcatgctaaaatccgcgatTCCGCCACGTCGCTCACCTTC
CAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCCAACTGGGGC**GCA**GGTACCCCAA
GCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCGACAAAAAATACTCGTACCGCGTCGTG
GTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAA
CTTCTCCAGTACAACAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTCGTTGTCTTTC
CAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 43)**
DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGI
DPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKVMGDDGVLACAIATHAKIRDSatsltf
qlaylvkkidfdytpnwgrg**a**gtpssyidnltfpkvltddkysyrvvngsdlgvesnfavtspgggtin
flqynkgygvadtktiqvfvpdgtgnseeyiaewkkt **(SEQ ID NO: 44)**

Der p 2-FveT29A (two-in-one chimeric mutant)

gatcaagtcgatgtcaaagattgtgccaatcatgaaatcaaaaaagttttggtaccaggatgccatgg
ttcagaaccatgtatcattcatcggtgtaaacattccaattggaagccgttttcgaagccaacaaa
acacaaaaacggctaaaattgaaatcaaagcctcaatcgatggtttagaagttgatgttcccggatc
gatccaaatgcatgccattacatgaaatgccattggttaaaggacaacaatatgatattaaatatac
atggaatgttccgaaaattgcacaaaaatctgaaaatggtgtcgctcactgttaaagttatgggtgatg
atggtgttttggcctgtgctattgctactcatgctaaaatccgcgatTCCGCCACGTCGCTCACCTTC
CAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCCAACTGGGGCCGTGGT**GCA**CCAA
GCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCGACAAAAAATACTCGTACCGCGTCGTG
GTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAA
CTTCTCCAGTACAACAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTCGTTGTCTTTC
CAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 45)**
DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGI
DPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKVMGDDGVLACAIATHAKIRDSatsltf
qlaylvkkidfdytpnwgrg**a**pssyidnltfpkvltddkysyrvvngsdlgvesnfavtspgggtin
flqynkgygvadtktiqvfvpdgtgnseeyiaewkkt **(SEQ ID NO: 46)**

Blo t 5-Der p 2-FveR27A (three-in-one chimeric mutant)

caagagcacaagccaagaaggatgatttccgaaacgaattcgatcacttggtgatcgaacaggcaaa
ccatgctatcgaaaaggagaaacatcaattgctttacttgcaacaccaactcgacgaattgaatgaaa
acaagagcaaggaattgcaagagaaaatcattcgagaacttgatgttggttgcgcatgatcgaagga
gccaaggagcttgggaacgtgaattgaagcgaactgatcttaacatttgggaacgattcaactacga
agaggctcaaactctcagcaagatcttgcttaaggatttgaaggaaaccgaacaaaagtgaaggata
ttcaaaccgaagatcaagtcgatgtcaaagattgtgccaatcatgaaatcaaaaaagttttggtacca
ggatgccatggttcagaaccatgtatcattcatcggtgtaaacattccaattggaagccgttttcga
agccaacaaaaacacaaaaacggctaaaattgaaatcaaagcctcaatcgatggtttagaagttgatg
ttcccggatcgatccaaatgcatgccattacatgaaatgccattggttaaaggacaacaatatgat
attaaatatacatggaatgttccgaaaattgcacaaaaatctgaaaatggtgtcgctcactgttaaagt

tatgggtgatgatgggtgttttggcctgtgctattgctactcatgctaaaatccgcgatTCCGCCACGT
CGCTCACCTTCCAGCTTGCCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCCCAACTGGGGC**GC**
AGGTACCCCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCGACAAAAATACTCGT
ACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGG
CAGACCATCAACTTCTCCAGTACAACAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTT
CGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA
(SEQ ID NO: 47)
QEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQDELNENKSKELQEKIIRELDVVCAMIEG
AQQALERELKRTDLNILERFNYEEAQTLKILLKDLKETEQKVVDIQTQDQVDVKDCANHEIKKVLVP
GCHGSEPCIHRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYMKCPLVKGQQYD
IKYTWNVPKIAPKSENVVVTVKVMGDDGVLACAIATHAKIRDSatsltfqlaylvkkidfdytpnwga
gtpssyidnltfpkvltddkysyrvvngsdlgvesnfavtppsggqtinflqynkgygvadtktiqvf
vvipdtgnseeyiaewkkt **(SEQ ID NO: 48)**

FUSION PROTEINS OF VIRAL ANTIGEN AND FVE

HPV E7-FveT29A

MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPPDRAHYNIVTFCKCDSTLRLC
VQSTHVDIRTLEDLLMGTLGIVCPICSQKPsatsltfqlaylvkkidfdytpnwgrgapssyidnltf
pkvltddkysyrvvngsdlgvesnfavtppsggqtinflqynkgygvadtktiqfvvipdtgnseey
iaewkkt **(SEQ ID NO: 49)**
atgcatggagatacacctacattgcatgaatatatgttagatttgcaaccagagacaactgatctcta
ctgttatgagcaattaaatgacagctcagaggaggaggatgaaatagatggtccagctggacaagcag
aaccggacagagcccattacaatattgtaacctttgttgcaagtgtgactctacgcttcggttggtgc
gtacaaagcacacacgtagacattcgtactttggaagacctgttaatgggcacactaggaattgtgtg
ccccatctgttctcagaaaccaTCCGCCACGTCGCTCACCTTCCAGCTTGCCCTACTTGGTGAAGAAGA
TCGACTTCGACTACACCCCCAACTGGGGCCGTGGTGCACCAAGCAGCTACATCGACAACCTTACCTTC
CCCAAGGTTCTCACCGACAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGA
GTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCTCCAGTACAACAAGGGGTATG
GTGTCGCGGACACCAAAACGATTCAAGTTTTCTGTTGTCATTCCAGATACCGGCAACTCGGAGGAGTAC
ATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 50)**

HCV Core23-FveT29A

Deletion of the 23 amino acids of core antigen from 141-163 amino acid residues
leads to increased protein production efficiency

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKA
RQPEGRAWAQPYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGY
LPLVYATGNLPGCSFSIFLLALLSCLTIPASAsatsltfqlaylvkkidfdytpnwgrgapssyidnlt
tfpkvltddkysyrvvngsdlgvesnfavtppsggqtinflqynkgygvadtktiqfvvipdtgnse
eyiaewkkt **(SEQ ID NO: 51)**
atgagcacgaatcctaaccctcaaagaaaaaccaaagcgaacaccaaccgcccacaggacgtcaa
gttcccggggcgggtggatcgatcggtcggtggagtttacctgttgccgcgcaggggccccaggttgggtg
tgccgcgcgactaggaagacttccgagcggctcgcaacctcgtggaaggcgacaacctatccccagggt
cgccagcccaggggtagggcctgggtcagccgggtacccctggccctctatggcaatgagggtt
ggggtgggcaggatggctcctgtcaccccggtggtcctcggcctagttggggccccacggacccccggc

gtaggtcgcgcaatttgggtaaggtcatcgataccctcacgtgcggttcgcccgatctcatgggggtac
cttcgctcgctcggcgcaacaggggaatctgccgggtgctccttttctatcttccttttggctttgct
gtcctgtttgaccatcccagcttcgcttatgaagTCCGCCACGTCGCTCACCTTCCAGCTTGCCTAC
TTGGTGAAGAAGATCGACTTCGACTACACCCCCAACTGGGGCCGTGGTGCACCAAGCAGCTACATCGA
CAACCTTACCTTCCCCAAGGTTCTCACCACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTG
ACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTAC
AACAAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTCGTTGTCATTCCAGATACCGGCAA
CTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 52)**

FUSION PROTEINS OF TUMOR-ASSOCIATED ANTIGEN AND FVE

MAGE3-FveT29A

mpleqrsqhckpeegleargealglvgaqapateeeqaasssstlvevtlgevpaaesppppqspqga
sslpttmnyplwsqsyedssnqeegpstfpdlesefqaalsrkvaelvfhlllkyrarepvtkaeml
gsvvgnwqyffpviskassslqlvfgielmevdpighlyifatclgltsydgllgdnqimpkagllii
vlaiaaregdcapeekiweelsvlevfegredsildgpkllltqhfvgenyleyrqvpgsdpacyefl
wgpralvetsykvvlhmvkissgpphisypplhewvlregeesatsltfqlaylvkkidfdytpnwgr
gapssyidnltfpkvltddkysyrvvngsdlgvesnfavtppsggqtinflqynkgygvadtktiqvf
vviptdgnseeyiaewkkt **(SEQ ID NO: 53)**

atgcctcttgagcagaggagtcagcactgcaagcctgaagaaggccttgaggccccgaggagaggccct
gggcctggtgggtgcgcaggctcctgctactgaggagcaggaggtgcctcctcctcttctactctag
ttgaagtcaccctgggggaggtgcctgctgccgagtcaccagatcctcccagagtcctcaggagacc
tccagcctcccactaccatgaactaccctctctggagccaatcctatgaggactccagcaaccaaga
agaggaggggccaagcaccttcctgacctggagtcagggttccaagcagcactcagtaggaagggtgg
ccgagttggttcattttctgctcctcaagtatcgagccaggagccgggtcacaaaggcagaaatgctg
gggagtgctcgtcggaaattggcagtatcttcttctctgtgatcttcagcaaagcttccagttccttgca
gctggtccttggcatcgagctgatggaagtggaccccatcgccacttgtagatcttggccacctgcc
tgggcctctcctacgatggcctgctgggtgacaatcagatcatgcccaggcaggcctcctgataatc
gtcctggccataatcgcaagagagggcgactgtgcccctgaggagaaaatctgggaggagctgagtg
gttagaggtgtttgaggggaggggaagacagtatcttgggggatcccaagaagctgctcaccacaactt
tcgtgcaggaaaactacctggagtaccggcagggtcccggcagtgatcctgcatgttatgaattcctg
tggggtccaagggccctcgttgaaaccagctatgtgaaagtcctgcaccataggttaaagatcagtg
aggacctcacatttctaccacacctgcatgagtggttttgagagaggggggaagagTCCGCCACGT
CGCTCACCTTCCAGCTTGCCTACTTGGTGAAGAAGATCGACTTCGACTACACCCCCAACTGGGGCCGT
GGTGCACCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGTTCTCACCACAAAAAATACTCGTA
CCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAACCTTCGCAGTGACACCGTCCGGTGGGC
AGACCATCAACTTCCTCCAGTACAACAAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTC
GTTGTCATTCCAGATACCGGCAACTCGGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ
ID NO: 54)**

MART1-FveT29A

mpredahfiygyppkghghsyttaeaaagigiltvilgvliligwycrrrngyralmdkslhvgtqc
altrrcpqegfdhrdskvslqekncepvvpnapayeklsaeqspypspatsltfqlaylvkkidf
dytpnwgrgapssyidnltfpkvltddkysyrvvngsdlgvesnfavtppsggqtinflqynkgygva
dtktiqvfviptdgnseeyiaewkkt **(SEQ ID NO: 55)**
atgccaagagaagatgctcacttcatctatggttaccccaagaaggggcacggccactcttacaccac
ggctgaagaggccgctgggatcgccatcctgacagtgatcctgggagttctactgctcatcggtgtt
ggtattgtagaagacgaaatggatacagagccttgatggataaaagtcttcatgttggcactcaatgt
gccttaacaagaagatgccacaagaagggttgatcatcgggacagcaagtgtctcttcaagagaa
aaactgtgaacctgtggttcccaatgctccacctgcttatgagaaactctctgcagaacagtccacc

caccttattcacctTCCGCCACGTCGCTCACCTTCCAGCTTGCTACTTGGTGAAGAAGATCGACTTC
GACTACACCCCCAACTGGGGCCGTGGTGCACCAAGCAGCTACATCGACAACCTTACCTTCCCCAAGGT
TCTCACCGACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACCTTGGCGTCGAGTCCAAC
TCGCAGTGACACCGTCCGGTGGGCAGACCATCAACTTCTCCAGTACAACAAGGGGTATGGTGTGCGG
GACACCAAAACGATTCAAGTTTTCGTTGTTCATTCAGATACCGGCAACTCGGAGGAGTACATCATCGC
TGAGTGGAAGAAGACTTGA (SEQ ID NO: 56)

CEA-FvøT29A

kltiestpfnvaegkevl1lvhnlpqhlfgywykgervdgnrqiigyviggtqqatpgpaysgreiiy
pnaslliqniiqndtgfytlhvksdlvneeatgqfrvypelpkpsissnnskpvedkdavaftepe
tqdatylwvnnqslpvsprlqlsngnrtltlfnvtrndtasykcetqnpvsarrsdsilnvlygpd
aptisplntsyrsgenlnlschaasnppaqyswfvngtfqgstqelfipnltvnnsgsytcqahnsdt
glrrttvtitvyaepkpfitssnnsnpvededavaltcepeiqttylwvnnqslpvsprlqls
nrtltllsvtrndvgpyecgignelsvdhsdpilnvlygpdptispsytyrpgvnslschaasn
ppaqyswldigniqtqelfisniteknsglytcqannsasghsrttvktitvsaelpkpsissnns
kpvedkdavaftepeaqttylwvnnqslpvsprlqlsngnrtltlfnvtrndarayvcgignsvs
anrsdpvtldvlygpdtpiispddssylsganlnlschsasnpqyswringipqghtqvlfiakit
pnngtyacfvsnlatgrnnsivksitvsasgtspglsagatvgimigvlvgvalisatsltfqlayl
vkkidfdytpnwgrgapssyidnltfpkvltddkysyrvvvngsdlgvesnfavtpsggqtinlfqyn
kgygvadtktiqvfvvipdtgnseeyiiaewkkt (SEQ ID NO: 57)

aagctcactattgaatccacgcggttcaatgtcgcagaggggaaggaggtgcttctacttgtccacaa
tctgccccagcatcttttggctacagctggtacaaaggtgaaagagtggatggcaaccgtcaaatta
taggatatgtaataggaactcaacaagctacccagggcccgcatcacagtggtcgagagataatatac
cccaatgcatccctgctgatccagaacatcatccagaatgacacaggattctacaccctacacgtcat
aaagtcatatcttgtgaatgaagaagcaactggccagttccgggtatacccgagctgccaagccct
ccatctccagcaacaactccaaaccgtggaggacaaggatgctgtggccttcacctgtgaacctgag
actcaggacgcaacctacctgtggtgggtaacaatcagagcctcccggtcagtcacaggctgcagct
gtccaatggcaacaggaccctcactctattcaatgtcacaagaaatgacacagcaagctacaaatgtg
aaaccagaacccagtgagtgcaggcgagtgattcagtcattcctgaatgtcctctatggcccgat
gccccaccatttcccctctaaacacatcttacagatcaggggaaaatctgaacctctcctgccatgc
agcctctaaccacactgcacagtagctcttgggttgtcaatgggactttccagcaatccaccaagagc
tctttatccccaacatcactgtgaataatagtggtatcctatacgtgccaagcccataactcagacact
ggcctcaataggaccacagtcacgacgatcacagtcctatgcagagccacccaaacccttcacaccag
caacaactccaaccccggtggaggatgaggatgctgtagccttaacctgtgaacctgagattcagaaca
caacctacctgtggtgggtaataatcagagcctcccggtcagtcacaggctgcagctgtccaatgac
aacaggaccctcactctactcagtggtcacaaggaatgatgtaggaccctatgagtggtgaatccagaa
cgaattaagtgttgaccacagcgaccagtcattcctgaatgtcctctatggccagacgacccccacca
ttccccctcatacacctattaccgtccaggggtgaacctcagcctctcctgccatgcagcctctaac
ccactgcacagtagtcttggctgattgatgggaacatccagcaacacacacaagagctctttatctc
caacatcactgagaagaacagcgagctctatacctgccaggccaataactcagccagtgccacagca
ggactacagtcagacaatcacagtcctctgcggagctgcccagccctccatctccagcaacaactcc
aaaccgtggaggacaaggatgctgtggccttcacctgtgaacctgaggctcagaacacaacctacct
gtggtgggtaaatggtcagagcctcccagtcagtcacaggctgcagctgtccaatggcaacaggacc
tcactctattcaatgtcacaagaaatgacgcaagagcctatgtatgtggaatccagaactcagtgagt
gcaaaccgcagtgaccagtcaccctggatgtcctctatgggcccggacacccccatcatttcccccc
agactcgtcttacctttcgggagcgaacctcaacctctcctgccactcggcctctaaccatccccgc
agtattcttggcgtatcaatgggataccgcagcaacacacacaagttctctttatcgccaaaatcacg
ccaaataataacgggacctatgcctgtttgtcttaacttggctactggccgcaataattccatagt
caagagcatcacagtcctctgcatctggaacttctcctggtctctcagctggggccactgtcggcac
tgattggagtgctggttggggtgctctgataTCCGCCACGTCGCTCACCTTCCAGCTTGCTACTTG
GTGAAGAAGATCGACTTACACCCCCAACTGGGGCCGTGGTGCACCAAGCAGCTACATCGACAA

CCTTACCTTCCCCAAGGTTCTCACCGACAAAAAATACTCGTACCGCGTCGTGGTCAATGGCTCTGACC
TTGGCGTCGAGTCCAACCTTCGAGTGACACCGTCCGGTGGGCAGACCATCAACTTCCTCCAGTACAAC
AAGGGGTATGGTGTGCGGGACACCAAAACGATTCAAGTTTTTCGTTGTCATTCCAGATACCGGCAACTC
GGAGGAGTACATCATCGCTGAGTGGAAGAAGACTTGA **(SEQ ID NO: 58)**

PRIMERS FOR CONSTRUCTION OF FIVE DELETION MUTANTS

Fd6-18F (36 mer)

5' -ggA/TCC/TCC/gCC/ACg/TCg/TTC/gAC/TAC/ACC/CCC/AAC- 3' **(SEQ ID NO: 59)**

Fd6-18R (36 mer)

5' -gTT/ggg/ggT/gTA/gTC/gAA/CgA/CgT/ggC/ggA/ggA/TCC- 3' **(SEQ ID NO: 60)**

Fd19-33F (36 mer)

5' -TTg/gTg/AAg/AAg/ATC/gAC/ATC/gAC/AAC/CTT/ACC/TTC- 3' **(SEQ ID NO: 61)**

Fd19-33R (36 mer)

5' -gAA/ggT/AAg/gTT/gTC/gAT/gTC/gAT/CTT/CTT/CAC/CAA- 3' **(SEQ ID NO: 62)**

Fd34-46F (36 mer)

5' -ggT/ACC/CCA/AgC/AgC/TAC/AAA/TAC/TCg/TAC/CgC/gTC- 3' **(SEQ ID NO: 63)**

Fd34-46R (36 mer)

5' -gAC/gCg/gTA/CgA/gTA/TTT/gTA/gCT/gCT/Tgg/ggT/ACC- 3' **(SEQ ID NO: 64)**

Fd47-60F (36 mer)

5' -AAg/gTT/CTC/ACC/gAC/AAA/gTC/gAg/TCC/AAC/TTC/gCA- 3' **(SEQ ID NO: 65)**

Fd47-60R (36 mer)

5' -TgC/gAA/gTT/ggA/CTC/gAC/TTT/gTC/ggT/gAg/AAC/CTT- 3' **(SEQ ID NO: 66)**

Fd61-72F (36 mer)

5' -AAT/ggC/TCT/gAC/CTT/ggC/CAg/ACC/ATC/AAC/TTC/CTC- 3' **(SEQ ID NO: 67)**

Fd61-72R (36 mer)

5' -gAg/gAA/gTT/gAT/ggT/CTg/gCC/AAg/gTC/AgA/gCC/ATT- 3' **(SEQ ID NO: 68)**

Fd73-84F (36 mer)

5' -gTg/ACA/CCg/TCC/ggT/ggg/ggT/gTC/gCg/gAC/ACC/AAA- 3' **(SEQ ID NO: 69)**

Fd73-84R (36 mer)

5' -TTT/ggT/gTC/CgC/gAC/ACC/CCC/ACC/ggA/Cgg/TgT/CAC- 3' **(SEQ ID NO: 70)**

Fd85-97F (36 mer)

5' -CAg/TAC/AAC/AAg/ggg/TAT/ATT/CCA/gAT/ACC/ggC/AAC- 3' **(SEQ ID NO: 71)**

Fd85-97R (36 mer)

5' -gTT/gCC/ggT/ATC/Tgg/AAT/ATA/CCC/CTT/gTT/gTA/CTg- 3' **(SEQ ID NO: 72)**

Fd98-106F (36 mer)

5' -ATT/CAA/gTT/TTC/gTT/gTC/TAC/ATC/ATC/gCT/gAg/Tgg- 3' **(SEQ ID NO: 73)**

Fd98-106R (36 mer)

5' -CCA/CTC/AgC/gAT/gAT/gTA/gAC/AAC/gAA/AAC/TTg/AAT- 3' **(SEQ ID NO: 74)**

Fd107-115R (39 mer)

5' -gAT/gCA/ACT/gAA/TTC/TTA/TTA/CTC/CTC/CgA/gTT/gCC/ggT- 3' **(SEQ ID NO: 75)**

PRIMERS FOR CONSTRUCTION OF LARGE FRAGMENT DELETION OF FVE

d(61-97)-F (36mer)

5' -/AAT/ggC/TCT/gAC/CTT/ggC/ATT/CCA/gAT/ACC/ggC/AAC/-3' **(SEQ ID NO: 76)**

d(61-97)-R (36mer)

5' -/gTT/gCC/ggT/ATC/Tgg/AAT/gCC/AAg/gTC/AgA/gCC/ATT/-3' **(SEQ ID NO: 77)**

PRIMERS FOR CONSTRUCTION OF SMALL FRAGMENT OF FVE (FROM 55AA TO 100AA)

[Fv55-100]-F (48mer)

5' -
/gTT/CCg/CgT/ggA/TCC/ATC/gAA/ggT/CgT/AAT/ggC/TCT/gAC/CTT/ggC/gTC/-3' **(SEQ ID NO: 78)**

[Fv55-100]-R (42mer)

5' -/gAT/gCA/ACT/gAA/TTC/TTA/TCA/ATC/Tgg/AAT/gAC/AAC/gAA/AAC/-3' **(SEQ ID NO: 79)**

PRIMERS FOR CONSTRUCTION OF POINT MUTANTS OF FVE

F(R27A)-F (27 mer)

5' - CCC/AAC/Tgg/ggC/gCA/ggT/ACC/CCA/AgC - 3' **(SEQ ID NO: 80)**

F(R27A)-R (27 mer)

5' - gCT/Tgg/ggT/ACC/TgC/gCC/CCA/gTT/ggg - 3' **(SEQ ID NO: 81)**

F(G28A)-F (27 mer)

5' - AAC/Tgg/ggC/CgT/gCA/ACC/CCA/AgC/AgC - 3' **(SEQ ID NO: 82)**

F(G28A)-R (27 mer)

5' - gCT/gCT/Tgg/ggT/TgC/ACg/gCC/CCA/gTT - 3' **(SEQ ID NO: 83)**

F(T29A)-F (27 mer)

5' - Tgg/ggC/CgT/ggT/gCA/CCA/AgC/AgC/TAC - 3' **(SEQ ID NO: 84)**

F(T29A)-R (27 mer)

5' - gTA/gCT/gCT/Tgg/TgC/ACC/ACg/gCC/CCA - 3' **(SEQ ID NO: 85)**

PRIMERS FOR BLO T 5-FVE FUSION PROTEIN

Bt5Fv-F (36mer)

5' - /AAg/gAT/ATT/CAA/ACC/CAA/TCC/gCC/ACg/TCg/CTC/ACC/-3' **(SEQ ID NO: 86)**

Bt5Fv-R (36mer)

5' - /ggT/gAg/CgA/CgT/ggC/ggA/TTg/ggT/TTg/AAT/ATC/CTT/-3' **(SEQ ID NO: 87)**

PRIMERS FOR DER P 2-FVE FUSION PROTEIN

Dp2Fv-F (36mer)

5' - /CAT/gCT/AAA/ATC/CgC/gAT/TCC/gCC/ACg/TCg/CTC/ACC-3' **(SEQ ID NO: 88)**

Dp2Fv-R (36mer)

5' - /ggT/gAg/CgA/CgT/ggC/ggA/ATC/gCg/gAT/TTT/AgC/ATg-3' **(SEQ ID NO: 89)**

PRIMERS FOR BLO T 5-DER P 2-FVE FUSION PROTEIN

Bt5Dp2-F (36mer)

5' - /aag/gat/att/caa/acc/caa/gat/caa/gtc/gat/gtc/aaa/-3' **(SEQ ID NO: 90)**

Bt5Dp2-R (36mer)

5' - /ttt/gac/atc/gac/ttg/atc/ttg/ggt/ttg/aat/atc/ctt/-3' **(SEQ ID NO: 91)**

Please delete the Appendix B header on page 172, and replace it with the following header:

APPENDIX B: FVE FRAGMENTS (RGT TRIPLET HIGHLIGHTED)

(APPENDIX DISCLOSES SEQ ID NOS: 92-487, RESPECTIVELY, IN ORDER OF APPEARANCE.)